IN THE CLAIMS:

Please amend claims 1 and 34 as follows:

1. (Currently Amended) A compound comprising two or more antigen binding regions linked to at least one prodrug-activating enzyme, wherein

a) the antigen binding regions consist of a single polypeptide chain;

b) the single polypeptide chain is comprised of a first variable domain, a second variable domain, and a polypeptide linker connecting the first variable domain and the second variable domain~~;~~, wherein a nucleotide sequence encoding the polypeptide linker is formed by two partially overlapping PCR primers during a PCR reaction that links the first variable domain and the second variable domain; and wherein

~~c) a nucleotide sequence encoding the polypeptide linker is formed by two partially overlapping PCR primers during a PCR reaction that links the first variable domain and the second variable domain; and wherein~~

~~d)~~ c) the compound has a bivalent or a multivalent structure.

2. (Previously Presented) A compound as claimed in claim 1, wherein the compound further comprises covalently bonded carbohydrates.

3. (Previously Presented) A compound as claimed in claim 1, wherein at least one antigen binding region comprises a variable domain of a heavy antibody chain and a variable domain of a light antibody chain (sFv fragment).

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4. (Original) A compound as claimed in claim 1, wherein the antigen binding region binds to a tumor-associated antigen (TAA).

5. (Previously Presented) A compound as claimed in claim 4, wherein the TAA is selected from the group consisting of an N-CAM, PEM, EGF-R, Sialyl-Le^a, Sialyl-Le^X, TFβ, GICA, GD_3, GD_2, TAG72, CA125, the 24-25 kDa glycoprotein defined by Mab L6, and CEA.

6. (Previously Presented) A compound as claimed in claim 1, wherein the enzyme is selected from the group consisting of a lactamase, pyroglutamate aminopeptidase, D-aminopeptidase, oxidase, peroxidase, phosphatase, hydroxynitrile lyase, protease, esterase, carboxypeptidase and glycosidase.

7. (Previously Presented) A compound as claimed in claim 6, wherein the enzyme is a β-glucuronidase, which is selected from the group consisting of an *E. coli* β-glucuronidase, a *Kobayasia nipponica* β-glucuronidase, a *Secale cereale* β-glucuronidase and a human β-glucuronidase.

8. (Original) A compound as claimed in claim 1, wherein the antigen binding region is linked to the enzyme via a peptide linker.

9. (Previously Presented) A compound as claimed in claim 2, wherein glycosylation covalently bonds the carbohydrates to the compound, and the glycosylation takes place either by means of chemical methods or by a selection of suitable expression systems.

10. (Previously Presented) A compound as claimed in claim 1, which has undergone secretory expression in *Saccharomyces cerevisiae* or in *Hansenula polymorpha*.

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11. (Previously Presented) A compound as claimed in claim 1, which is expressed in *E. coli* and is subsequently chemically glycosylated.

12. (Previously Presented) A compound as claimed in claim 30, wherein the sFv-β-lactamase fusion protein has undergone periplasmic expression in *E. coli* and is chemically glycosylated.

13. (Previously Presented) A compound as claimed in claim 30, wherein the sFv-β-lactamase fusion protein has undergone secretory expression in *Saccharomyces cerevisiae* or *Hansenula polymorpha*.

14. (Withdrawn) A nucleic acid coding for a compound as claimed in claim 1.

15. (Withdrawn) A nucleic acid as claimed in claim 14, coding for a humanized sFv fragment against CEA and a human β-glucuronidase.

16. (Withdrawn) A nucleic acid as claimed in claim 14 with the sequence

```
CCAAGCTTAT GAATATGCAA ATCCTGCTCA TGAATATGCA AATCCTCTGA          50

ATCTACATGG TAAATATAGG TTTGTCTATA CCACAAACAG AAAAACATGA         100

GATCACAGTT CTCTCTACAG TTACTGAGCA CACAGGACCT  CACC ATG GGA TGG  153
                                                 Met Gly  Trp
AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGTAAGGGGC     199
Ser  Cys Ile  Ile  Leu  Phe Leu Val  Ala  Thr  Ala  Thr
                          -10
TCACAGTAGC AGGCTTGAGG TCTGGACATA TATATGGGTG ACAATAGACAT        249

CCACTTTGCC TTTCTCTCCA CA GGT GTC CAC TCC CAG GTC CAA CTG CAG    298
                          Gly Val His Ser Gln Val Gln Leu Gln
                                                1
GAG AGC GGT CCA GGT CTT GTG AGA CCT AGC CAG ACC CTG AGC CTG     343
Glu Ser Gly  Pro  Gly  Leu Val  Arg Pro  Ser  Gln Thr  Leu Ser  Leu
                    10
ACC TGC ACC GTG TCT GGC TTC ACC ATC AGC AGT GGT TAT AGC TGG     388
Thr Cys  Thr  Val  Ser  Gly  Phe Thr  Ile  Ser  Ser  Gly  Tyr Ser  Trp
                                          30
CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT GAG TGG ATT GGA     433
His Trp  Val  Arg  Gln  Pro Pro  Gly  Arg Gly  Leu Glu  Trp  Ile  Gly
                    40
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TAC ATA CAG TAC AGT GGT ATC ACT AAC TAC AAC CCC TCT CTC AAA          478
Tyr Ile  Gln Tyr Ser Gly Ile  Thr Asn  Tyr Asn  Pro Ser Leu Lys
                                  60
AGT AGA GTG ACA ATG CTG GTA GAC ACC AGC AAG AAC CAG TTC AGC          523
Ser Arg Val  Thr Met Leu Val Asp  Thr Ser Lys Asn Gln Phe Ser
                70                                  80
CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC TAT TAT          568
Leu Arg Leu Ser Ser Val Thr Ala  Ala Asp  Thr Ala Val Tyr Tyr
                                  90
TGT GCA AGA GAA GAC TAT GAT TAC CAC TGG TAC TTC GAT GTC TGG          613
Cys Ala  Arg Glu Asp  Tyr Asp  Tyr His  Trp Tyr  Phe Asp Val  Trp
                100                                 110
GGC CAA CCC ACC ACG GTC ACC GTC TCC TCA GGA GGC GGT GGA TCG          658
Gly Gln  Gly Thr  Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
                                 120
GGC GGT GGT GGG TCG GGT GGC GGC GGA TCT GAC ATC CAG CTG ACC          703
Gly Gly  Gly Gly  Ser Gly Gly  Gly Gly  Ser Asp  Ile  Gln Leu Thr
                130                                 140
CAG AGC CCA AGC AGC CTG AGC GCC AGC CTC GGT GAC AGA GTG ACC          748
Gln Ser  Pro Ser  Ser Leu Ser Ala  Ser Val Gly  Asp Arg Val  Thr
                                 150
ATC ACC TGT AGT ACC AGC TCG AGT GTA AGT TAC ATG CAC TGG TAC          793
Ile  Thr Cys Ser  Thr Ser  Ser Ser Val  Ser Tyr Met  His Trp Tyr
                160                                 170
CAG CAG AAG CCA GGT AAG GCT CCA AAG CTG CTG ATC TAC AGC ACA          838
Gln Gln  Lys Pro  Gly Lys Ala  Pro Lys Leu  Leu Ile  Tyr Ser Thr
                                 180
TCC AAC CTG GCT TCT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT          883
Ser Asn  Leu Ala  Ser Gly  Val  Pro Ser Arg  Phe Ser  Gly Ser Gly
                190                                 200
AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG          928
Ser Gly  Thr Asp  Phe Thr  Phe Thr  Ile  Ser Ser  Leu Gln  Pro Glu
                                 210
GAC ATC GCC ACC TAC TAC TGC CAT CAG TGG AGT AGT TAT CCC ACG          973
Asp Ile  Ala Thr  Tyr Tyr  Cys His Gln  Trp Ser Ser  Tyr Pro Thr
                220                                 230
TTC GGC CAA GGG ACC AAG CTG GAG ATC AAA GGTGAGTAGA ATTTAAACTTT      1023
Phe Gly  Gln Gly  Thr Lys Leu Glu  Ile Lys
                                 240
TGCTTCCTCA GTTGGATCTG AGTAACTCCC AATCTTCTCT CTGCA GAG CTC AAA      1077
                                                  Glu Leu Lys

ACC CCA CTT GGT GAC ACA ACT CAC ACA TGC CCA CGG TGC CCA            1119
Thr Pro  Leu Gly  Asp  Thr Thr His  Thr  Cys Pro Arg  Cys Pro
                                 250
GGTAAGCCAG CCCAGGACTC GCCCTCCAGC TCAAGGCGGG ACAAGAGCCC            1169

TAGAGTGGCC TGAGTCCAGG GACAGGCCC AGCAGGGTGC TGACGCATCC             1219
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ACCTCCATCC CAGATCCCCG TAACTCCCAA TCTTCTCTCT GCA GCG GCG GCG 1271
Ala Ala Ala
260
GCG GTG CAG GGC GGG ATG CTG TAC CCC CAG GAG AGC CCG TCG CGG 1316
Ala Val Gln Gly Gly Met Leu Tyr Pro Gln Glu Ser Pro Ser Arg
270
GAG TGC AAG GAG CTG GAC GGC CTC TGG AGC TTC CGC GCC GAC TTC 1361
Glu Cys Lys Glu Leu Asp Gly Leu Trp Ser Phe Arg Ala Asp Phe
280 290
TCT GAC AAC CGA CGC CGG GGC TTC GAG GAG CAG TGG TAC CGG CGG 1406
Ser Asp Asn Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg
300
CCG CTG TGG GAG TCA GGC CCC ACC GTG GAC ATG CCA GTT CCC TCC 1451
Pro Leu Trp Glu Ser Gly Pro Thr Val Asp Met Pro Val Pro Ser
310 320
AGC TTC AAT GAC ATC AGC CAG GAC TGG CGT CTG CGG CAT TTT GTC 1496
Ser Phe Asn Asp Ile Ser Gln Asp Trp Arg Leu Arg His Phe Val
330
GGC TGG GTG TGG TAC GAA CGG GAG GTG ATC CTG CCG GAG CGA TGG 1541
Gly Trp Val Trp Tyr Glu Arg Glu Val Ile Leu Pro Glu Arg Trp
340 350
ACC CAG GAC CTG CGC ACA AGA GTG GTG CTG AGG ATT GGC AGT GCC 1586
Thr Gln Asp Leu Arg Thr Arg Val Val Leu Arg Ile Gly Ser Ala
360
CAT TCC TAT GCC ATC GTG TGG GTG AAT GGG GTC GAC ACG CTA GAG 1631
His Ser Tyr Ala Ile Val Trp Val Asn Gly Val Asp Thr Leu Glu
370 380
CAT GAG GGG GGC TAC CTC CCC TTC GAG GCC GAC ATC AGC AAC CTG 1676
His Glu Gly Gly Tyr Leu Pro Phe Glu Ala Asp Ile Ser Asn Leu
390
GTC CAG GTG GGG CCC CTG CCC TCC CGG CTC CGA ATC ACT ATC GCC 1721
Val Gln Val Gly Pro Leu Pro Ser Arg Leu Arg Ile Thr Ile Ala
400 410
ATC AAC AAC ACA CTC ACC CCC ACC ACC CTG CCA CCA GGG ACC ATC 1766
Ile Asn Asn Thr Leu Thr Pro Thr Thr Leu Pro Pro Gly Thr Ile
420
CAA TAC CTG ACT GAC ACC TCC AAG TAT CCC AAG GGT TAC TTT GTC 1811
Gln Tyr Leu Thr Asp Thr Ser Lys Tyr Pro Lys Gly Tyr Phe Val
430 440
CAG AAC ACA TAT TTT GAC TTT TTC AAC TAC GCT GGA CTG CAG CGG 1856
Gln Asn Thr Tyr Phe Asp Phe Phe Asn Tyr Ala Gly Leu Gln Arg
450
TCT GTA CTT CTG TAC ACG ACA CCC ACC ACC TAC ATC GAT GAC ATC 1901
Ser Val Leu Leu Tyr Thr Thr Pro Thr Thr Tyr Ile Asp Asp Ile
460 470
ACC GTC ACC ACC AGC GTG GAG CAA GAC AGT GGG CTG GTG AAT TAC 1946
Thr Val Thr Thr Ser Val Glu Gln Asp Ser Gly Leu Val Asn Tyr
480
CAG ATC TCT GTC AAG GGC AGT AAC CTG TTC AAG TTG GAA GTG CGT 1991
Gln Ile Ser Val Lys Gly Ser Asn Leu Phe Lys Leu Glu Val Arg
490 500

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CTT TTG GAT GCA GAA AAC AAA GTC GTG GCG AAT GGG ACT GGG ACC 2036
Leu Leu Asp Ala Glu Asn Lys Val Val Ala Asn Gly Thr Gly Thr
510
CAG GGC CAA CTT AAG GTG CCA GGT GTC AGC CTC TGG TGG CCG TAC 2081
Gln Gly Gln Leu Lys Val Pro Gly Val Ser Leu Trp Trp Pro Tyr
520 530
CTG ATG CAC GAA CGC CCT GCC TAT CTG TAT TCA TTG GAG GTG CAG 2126
Leu Met His Glu Arg Pro Ala Tyr Leu Tyr Ser Leu Glu Val Gln
540
CTG ACT GCA CAG ACG TCA CTG GGG CCT GTG TCT GAC TTC TAC ACA 2171
Leu Thr Ala Gln Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr Thr
550 560
CTC CCT GTG GGG ATC CGC ACT GTG GCT GTC ACC AAG AGC CAG TTC 2216
Leu Pro Val Gly Ile Arg Thr Val Ala Val Thr Lys Ser Gln Phe
570
CTC ATC AAT GGG AAA CCT TTC TAT TTC CAC GGT GTC AAC AAG CAT 2261
Leu Ile Asn Gly Lys Pro Phe Tyr Phe His Gly Val Asn Lys His
580 590
GAG GAT GCG GAC ATC CGA GGG AAG GGC TTC GAC TGG CCG CTG CTG 2306
Glu Asp Ala Asp Ile Arg Gly Lys Gly Phe Asp Trp Pro Leu Leu
600
GTG AAG GAC TTC AAC CTG CTT CGC TGG CTT GGT GCC AAC GCT TTC 2351
Val Lys Asp Phe Asn Leu Leu Arg Trp Leu Gly Ala Asn Ala Phe
610 620
CGT ACC AGC CAC TAC CCC TAT GCA GAG GAA GTG ATG CAG ATG TGT 2396
Arg Thr Ser His Tyr Pro Tyr Ala Glu Glu Val Met Gln Met Cys
630
GAC CGC TAT GGG ATT GTG GTC ATC GAT GAG TGT CCC GGC GTG GGC 2441
Asp Arg Tyr Gly Ile Val Val Ile Asp Glu Cys Pro Gly Val Gly
640 650
CTG GCG CTG CCG CAG TTC TTC AAC AAC GTT TCT CTG CAT CAC CAC 2486
Leu Ala Leu Pro Gln Phe Phe Asn Asn Val Ser Leu His His His
660
ATG CAG GTG ATG GAA GAA GTG GTG CGT AGG GAC AAG AAC CAC CCC 2531
Met Gln Val Met Glu Glu Val Val Arg Arg Asp Lys Asn His Pro
670 680
GCG GTC GTG ATG TGG TCT GTG GCC AAC GAG CCT GCG TCC CAC CTA 2576
Ala Val Val Met Trp Ser Val Ala Asn Glu Pro Ala Ser His Leu
690
GAA TCT GCT GGC TAC TAC TTG AAG ATG GTG ATC GCT CAC ACC AAA 2621
Glu Ser Ala Gly Tyr Tyr Leu Lys Met Val Ile Ala His Thr Lys
700 710
TCC TTG GAC CCC TCC CGG CCT GTG ACC TTT GTG AGC AAC TCT AAC 2666
Ser Leu Asp Pro Ser Arg Pro Val Thr Phe Val Ser Asn Ser Asn
720
TAT GCA GCA GAC AAG GGG GCT CCG TAT GTG GAT GTG ATC TGT TTG 2711
Tyr Ala Ala Asp Lys Gly Ala Pro Tyr Val Asp Val Ile Cys Leu
730 740
AAC AGC TAC TAC TCT TGG TAT CAC GAC TAC GGG CAC CTG GAG TTG 2756
Asn Ser Tyr Tyr Ser Trp Tyr His Asp Tyr Gly His Leu Glu Leu
750

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ATT CAG CTG CAG CTG GCC ACC CAG TTT GAG AAC TGG TAT AAG AAG 2801
Ile Gln Leu Gln Leu Ala Thr Gln Phe Glu Asn Trp Tyr Lys Lys
760 770
TAT CAG AAG CCC ATT ATT CAG AGC GAG TAT GGA GCA GAA ACG ATT 2846
Tyr Gln Lys Pro Ile Ile Gln Ser Glu Tyr Gly Ala Glu Thr Ile
780
GCA GGG TTT CAC CAG GAT CCA CCT CTG ATG TTC ACT GAA GAG TAC 2891
Ala Gly Phe His Gln Asp Pro Pro Leu Met Phe Thr Glu Glu Tyr
790 800
CAG AAA AGT CTG CTA GAG CAG TAC CAT CTG GGT CTG GAT CAA AAA 2936
Gln Lys Ser Leu Leu Glu Gln Tyr His Leu Gly Leu Asp Gln Lys
810
CGC AGA AAA TAT GTG GTT GGA GAG CTC ATT TGG AAT TTT GCC GAT 2981
Arg Arg Lys Tyr Val Val Gly Glu Leu Ile Trp Asn Phe Ala Asp
820 830
TTC ATG ACT GAA CAG TCA CCG ACG AGA GTG CTG GGG ATT AAA AAG 3026
Phe Met Thr Glu Gln Ser Pro Thr Arg Val Leu Gly Asn Lys Lys
840
GGG ATC TTC ACT CGG CAG AGA CAA CCA AAA AGT GCA GCG TTC CTT 3071
Gly Ile Phe Thr Arg Gln Arg Gln Pro Lys Ser Ala Ala Phe Leu
850 860
TTG CGA GAG AGA TAC TGG AAG ATT GCC AAT GAA ACC AGG TAT CCC 3116
Leu Arg Glu Arg Tyr Trp Lys Ile Ala Asn Glu Thr Arg Tyr Pro
870
CAC TCA GTA GCC AAG TCA CAA TGT TTG GAA AAC AGC CCG TTT ACT 3161
His Ser Val Ala Lys Ser Gln Cys Leu Glu Asn Ser Pro Phe Thr
880 890
TGA GCAAGACTGA TACCACCTGC GTGTCCCTTC CTCCCCGAGT CAGGGCGACT 3214

TCCACAGCAG CAGACAAGT GCCTCCTGGA CTGTTCACGG CAGACCAGAA 3264

CGTTTCTGGC CTGGGTTTTG TGGTCATCTA TTCTAGCAGG GAACACTAAA 3314.

17. (Withdrawn) A vector containing a nucleic acid as claimed in claim 14.

18. (Withdrawn) A host cell containing a nucleic acid as claimed in claim 14 or a vector as claimed in claim 17.

19. (Withdrawn) A host cell as claimed in claim 18, which is a BHK, CHO, COS, HeLa, insect, tobacco plant, yeast or *E. coli* cell.

20. (Withdrawn) A transgenic mammal with the exception of a human, containing a DNA as claimed in claim 14 or a vector as claimed in claim 17.

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21. (Withdrawn) A process for preparing a compound as claimed in claim 1, which comprises

a) introducing a nucleic acid as claimed in claim 14 or a vector as claimed in claim 17 into a host cell,

b) cultivating the host cell, and

c) isolating the compound.

22. (Withdrawn) A process for preparing a compound as claimed in claim 1, which comprises

a) cultivating a host cell as claimed in claim 18, and

b) isolating the compound.

23. (Canceled).

24. (Canceled).

25. (Previously Presented) A pharmaceutical composition comprising a compound as claimed in claim 1 and a physiologically acceptable carrier.

26. (Previously Presented) A diagnostic aid comprising a compound as claimed in claim 1.

27. (Previously Presented) A compound as claimed in claim 6, wherein the lactamase enzyme is a *Bacillys cereus* β-lactamase II.

28. (Previously Presented) A compound as claimed in claim 6, wherein the carboxypeptidase enzyme is a carboxypeptidase G2 from *Pseudomonas*.

29. (Previously Presented) A compound as claimed in claim 10, which has undergone secretory expression in *Hansenula polymorpha*.

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30. (Previously Presented) A compound as claimed in claim 1, wherein at lease one antigen binding region and at least one prodrug-activating enzyme form an sFv-β-lactamase fusion protein.

31. (Previously Presented) A compound as claimed in claim 11, wherein the chemical glycosylation involves at least one of galactosylation or mannosylation.

32. (Previously Presented) A compound as claimed in claim 12, wherein the chemical glycosylation involves at least one of galactosylation or mannosylation.

33. (Previously Presented) A method of treating cancer comprising administering a compound claimed in claim 1 to a host in need thereof and subsequently administering a prodrug to be activated by the enzyme portion of the compound of claim 1.

34. (Currently Amended) A compound comprising one or more antigen binding regions linked to at least one prodrug-activating enzyme, wherein

a) the antigen binding regions consist of a single polypeptide chain;

b) the single polypeptide chain is comprised of a first variable domain, a second variable domain, and a polypeptide linker connecting the first variable domain and the second variable domain~~;~~, wherein a nucleotide sequence encoding the polypeptide linker is formed by two partially overlapping PCR primers during a PCR reaction that links the first variable domain and the second variable domain; and wherein

~~c) a nucleotide sequence encoding the polypeptide linker is formed by two partially overlapping PCR primers during a PCR reaction that~~

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~~links the first variable domain and the second variable domain; and~~

~~wherein~~

~~d)~~ c) the compound has a monovalent, bivalent, or multivalent structure.

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